Early detection of positive blood cultures using recurrent neural networks on time series data

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Abstract

The presence of bacteria or fungi in the bloodstream of patients can lead to life-threatening conditions. A computational model is developed to assist doctors in the intensive care unit (ICU) to predict whether blood cultures of patients will return positive. Our model is based on a Bi-directional Long Short-Term Memory (BiLSTM) artificial neural network. As input it uses nine monitored clinical parameters, presented as time series data, collected from 2000 ICU admissions at the Ghent University Hospital.

1. Introduction

A positive blood culture is defined as a blood sample where bacteria or fungi are present. This growth of organisms in the blood stream can lead to inflammation throughout the body or even organ failure or death (Morrell et al., 2005). When doctors suspect a patient to have a positive blood culture they can decide to advance to a blood culture test. Symptoms indicative of a likely positive culture are complex and not fully understood. Nevertheless, it is suspected a link exists between a patients physiological data and the outcome of such a test. This work presents research about how computational models can assist in detecting culture positive patients or even suggest new relationships.

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2. Data collection and processing

A database was constructed with physiological information from 2177 patients admitted at the ICU of the Gent University Hospital whereof 229 admissions had a positive blood culture test. For all other patients, a blood test was performed which returned negative. The dataset contains more than 14 million values associated with 29 parameters. Those variables can be subdivided and reduced to 9 parameter groups including blood pressure, temperature, resperatory rate, organ health assessments and blood count measurements. The data was further processed to exclude transcriptional errors and transformed into time series with a constant interval. This was done by by taking the last, mean, minimum or maximum parameter value in a set time window. A time series ends at the point when a first positive blood culture test is taken or in case of a negative culture patient, where there was no positive test, at the time when the physiological data flow stops.

3. Methods

A Recurrent Neural Network (RNN) is a computational model designed to work with temporal features. It is similar to a feed forward neural network by extension that cycles are present in the network. Through those cycles the model can obtain a memory effect that allows to learn using input from several time steps in the past.

A commonly recognized problem in training recurrent neural networks is the vanishing gradient problem. The influence of inputs from several time steps

Table 1. Prediction results of different networks trained on the last values.

NETWORK	ROC AUC	PR AUC
RNN	0.797	0.492
BIRNN	0.818	0.529
LSTM	0.837	0.453
BILSTM	0.841	0.499
BILSTM ADV.	0.891	0.629

away fades exponentially. This makes it impossible for those networks to learn longterm dependencies. Long Short-Term Memory (LSTM) networks (Hochreiter & Schmidhuber, 1997) mitigate this problem by introducing the the principle of gating. A gate makes it possible for the network to block inputs or outputs and that way contain the hidden state for longer time periods.

In our work, we have used five types of networks: A unidirectional RNN, a bidirectional RNN, a unidirectional LSTM network, a bidirectional LSTM (BiLSTM) network and a more complex BiLSTM network (BiLSTM adv.) with an extra hidden layer. In the more complex BiLSTM network, hidden states from all time steps have direct influence to the output node. In contrast, in the BiLSTM network, the hidden state values need to ripple through the whole LSTM chain. Figure 1 depicts an advanced BiLSTM network. All networks consist of 1000 hidden nodes. A weighted MSE cost function is used with more weight for positive admissions to compensate the imbalance in the dataset. There are about nine times more negative admissions than positive ones.

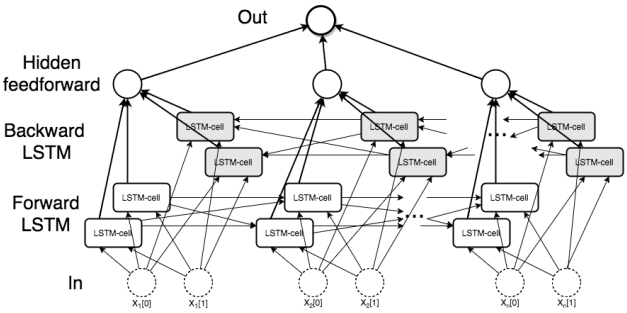

Figure 1. Topology of an unfolded BiLSTM network with 2 input features and 2 LSTM cells and an extra hidden feedforward layer.

4. Evaluation

This section handles the evaluation of the mentioned networks. Models are compared based on their ability to predict up to the point where an actual blood sample is taken and on their early prediction capabilities. Finally the temporal models are compared to a nontemporal one.

Table 1 shows the area under the Receiver Operator Characteristic and Precision Recall curve (ROC auc and PR auc). We use a dataset where the last value in a sample window is used. It is clear that the advanced BiLSTM network (BiLSTM adv.) achieved the best performance in this setting.

Diagnosing a culture positive patient earlier increases the chances of survival. Therefore the model was also tested on sequences that end several hours before the actual blood test was performed. The network is first trained on sequences that span 24 hours. Next, the network is tested on sequences that stopped x hours earlier. We conclude that up to 10 hours upfront the model still reaches a ROC auc of 0.8. At 24 hours upfront the ROC auc is around 0.76. The area under the precision recall curve shows a similar evolution.

It is interesting to see whether using temporal information actually brings an added value in predicting a blood culture test outcome. For this we compare to a feed forward neural network (FNN). As input we use an extremum dataset except that only the most recent sample is taken instead of the whole sequence. The BiLSTM network uses the dataset with last samples from each sample window. The FNN network keeps up with the BiLSTM at times close to the blood culture test but at 24 hours upfront the difference is already remarkable. This indicates that indeed the temporal models bring an advantage to the table.

5. Conclusion

This research explored models that are able to capture temporal effects and predict blood culture test outcomes. We conclude that temporal models are clearly better in predicting the outcome of a blood culture test than non-temporal models. Temporal models have a slight advantage in predicting the outcome close to the time the blood sample test was taken but are noticeably better than other models several hours upfront.

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